



2008-07-23 revised Seq List for filing
SEQUENCE LISTING

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
BURNOUF, Dominique, Yves, Joel
WAGNER, Jerome, Edouard
DUMAS, Philippe
FUJII, Shingo
FUCHS, Robert, Pierre, Paul
OLIERIC, Vincent

<120> PROTEIN CRYSTAL COMPRISING THE PROCESSIONITY CLAMP FACTOR OF DNA
POLYMERASE AND A LIGAND, AND ITS USES

<130> 0508-1147

<140> US 10/561,867
<141> 2006-07-06

<150> PCT/EP2004/006942
<151> 2004-06-25

<150> EP 03291596.9
<151> 2003-06-27

<160> 7

<170> PatentIn version 3.5

<210> 1
<211> 16
<212> PRT
<213> Escherichia coli

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1 5 10 15

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<211> 22
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic oligonucleotide - Control peptide

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Arg Pro Val Lys Val Thr Pro Asn Gly Ala Glu Asp Glu Ser Ala Glu
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Ala Phe Pro Leu Glu Phe
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<212> DNA
<213> Artificial sequence

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<223> synthetic oligonucleotide - Primer for replication assay

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<210> 4
<211> 90
<212> DNA
<213> Artificial sequence

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<223> synthetic oligonucleotide - Template for replication assay

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tttacaacgt cgtgactggg aaaaccctgg 90

<210> 5
<211> 366
<212> PRT
<213> Escherichia coli
<400> 5

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
115 120 125

Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe
130 135 140

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Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
145 150 155 160

Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165 170 175

Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser
180 185 190

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp
195 200 205

Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg
210 215 220

Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg
225 230 235 240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu
245 250 255

Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile
260 265 270

Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn
275 280 285

Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu
290 295 300

Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn
305 310 315 320

Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val
325 330 335

Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala
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Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu
355 360 365

<210> 6

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide - derived from SEQ ID NO 1

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<400> 6

Arg Gln Leu Val Leu Gly Leu
1 5

<210> 7

<211> 210

<212> PRT

<213> synthetic peptide - Artificial Sequence

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<223> derived from beta clamp of E. coli DNA polymerase III

<400> 7

Leu Asn Gly Met Leu Phe Glu Thr Glu Gly Glu Glu Leu Arg Thr Val
1 5 10 15

Ala Thr Asp Gly His Arg Leu Ala Val Cys Ser Met Pro Ile Gly Gln
20 25 30

Ser Leu Pro Ser His Ser Val Ile Val Pro Arg Lys Gly Val Ile Glu
35 40 45

Leu Met Arg Met Leu Asp Gly Gly Asp Asn Pro Leu Arg Val Gln Ile
50 55 60

Gly Ser Asn Asn Ile Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser
65 70 75 80

Lys Leu Val Asp Gly Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys
85 90 95

Asn Pro Asp Lys His Leu Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala
100 105 110

Phe Ala Arg Ala Ala Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg
115 120 125

Leu Tyr Val Ser Glu Asn Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu
130 135 140

Gln Glu Glu Ala Glu Glu Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu
145 150 155 160

Met Glu Ile Gly Phe Asn Val Ser Tyr Val Leu Asp Val Leu Asn Ala
165 170 175

Leu Lys Cys Glu Asn Val Arg Met Met Leu Thr Asp Ser Val Ser Ser
180 185 190

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Val Gln Ile Glu Asp Ala Ala Ser Gln Ser Ala Ala Tyr Val Val Met
195 200 205